

GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: March 17, 2003, 07:19:15 ; Search time 28.0916 Seconds
(without alignments)
234.715 Million cell updates/sec

Title: US-09-787-082-5

Perfect score: 190

Sequence: 1 CKGKGAKSRLMYDCTGSCRSRGKTRNGLPG 32

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_21.*

- 1: sp_archaea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mhc.*
- 8: sp_organelle.*
- 9: sp_phage.*
- 10: sp_plant.*
- 11: sp_rodent.*
- 12: sp_virus.*
- 13: sp_vertebrate.*
- 14: sp_unclassified.*
- 15: sp_rvirus.*
- 16: sp_bacteriap.*
- 17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	127	66.8	66	5 Q9N633	Q9N633 conus catus
2	127	66.8	66	5 Q9NCW6	Q9NCW6 conus catus
3	127	66.8	66	5 Q9NCW5	Q9NCW5 conus catus
4	127	66.8	66	5 Q9NCW3	Q9NCW3 conus catus
5	120	63.2	66	5 Q9NCW4	Q9NCW4 conus catus
6	120	63.2	66	5 Q9NCV5	Q9NCV5 conus catus
7	117	61.6	66	5 Q9NCV7	Q9NCV7 conus catus
8	116	61.1	66	5 Q9NCV6	Q9NCV6 conus catus
9	116	61.1	66	5 Q9NCV4	Q9NCV4 conus catus
10	116	61.1	66	5 Q9NCV0	Q9NCV0 conus catus
11	116	61.1	66	5 Q9NCU1	Q9NCU1 conus catus
12	115	60.5	66	5 Q9N628	Q9N628 conus catus
13	115	60.5	66	5 Q9N625	Q9N625 conus catus
14	115	60.5	66	5 Q9NCW2	Q9NCW2 conus catus
15	115	60.5	66	5 Q9NCV3	Q9NCV3 conus catus
16	115	60.5	66	5 Q9NCV2	Q9NCV2 conus catus

17	115	60.5	66	5 Q9NCV1	Q9NCV1 conus stria
18	114	60.0	66	5 Q9N6F7	Q9N6F7 conus catus
19	114	60.0	66	5 Q9NCW1	Q9NCW1 conus catus
20	104	54.7	66	5 Q9N6F8	Q9N6F8 conus catus
21	104	54.7	66	5 Q9NCW0	Q9NCW0 conus catus
22	104	54.7	66	5 Q9NCV9	Q9NCV9 conus catus
23	103	54.2	66	5 Q9NCV6	Q9NCV6 conus catus
24	95	50.0	66	5 Q9NCV8	Q9NCV8 conus catus
25	70	36.8	686	5 Q94316	Q94316 caenorhabdi
26	65.5	34.5	57	5 Q9N9H2	Q9N9H2 venerupis (
27	65.5	34.5	59	5 Q9N9H1	Q9N9H1 rudistapes d
28	65.5	34.5	80	5 Q9BIV4	Q9BIV4 crassostrea
29	65.5	34.5	107	5 Q9NG19	Q9NG19 crassostrea
30	64	33.7	600	13 Q9PVK7	Q9PVK7 naja naja (
31	63	33.2	401	13 P82942	P82942 naja naja k
32	62.5	32.9	75	5 Q9UIN5	Q9UIN5 crassostrea
33	61.5	32.4	105	13 Q93517	Q93517 agkistrodon
34	61.5	32.4	610	13 Q9DGB9	Q9DGB9 crotalus at
35	61	32.1	451	13 Q9PT49	Q9PT49 atractaspis
36	61	32.1	541	4 Q9H6L0	Q9H6L0 homo sapien
37	60	31.6	81	5 Q9BP83	Q9BP83 conus arena
38	60	31.6	604	13 Q9PT48	Q9PT48 atractaspis
39	59.5	31.3	751	5 Q01497	Q01497 caenorhabdi
40	59	31.1	78	5 Q9U656	Q9U656 conus texti
41	59	31.1	2447	5 Q9NEF9	Q9NEF9 drosophila
42	59	31.1	4072	5 Q9W4Y4	Q9W4Y4 drosophila
43	58	30.5	78	5 Q9U655	Q9U655 conus texti
44	57.5	30.3	1368	5 Q23821	Q23821 caenorhabdi
45	57	30.0	67	5 Q9N604	Q9N604 conus stria

ALIGNMENTS

RESULT 1

Q9N633 PRELIMINARY; PRT; 66 AA.
ID Q9N633;
AC Q9N633;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Four-loop conotoxin precursor (fragment).
OS Conus catus.
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
OX Neogastropoda; Conoidea; Conidae; Conus.
OX NCBI_TaxID=101291;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CCATH_11_6, CCATH_11_1, AND CCATH_11_2;
RT Duda T.F., Palumbi S.R.;
RT "Molecular evolution of four-loop conotoxin precursors from fish-eating Conus."
RL Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AF174219; AAF89883.1; -;
DR EMBL; AF174214; AAF89878.1; -;
DR EMBL; AF174215; AAF89879.1; -;
DR HSSP; P05484; 1MVI.
DR InterPro; IPR004214; Conotoxin.
DR Fram; PF02950; Conotoxin; 1.
FT NON_TER 1
SQ SEQUENCE 66 AA; 7053 MW; E445338A6968A1AC CRC64;

Query Match 66.8%; Score 127; DB 5; Length 66;
Best Local Similarity 80.0%; Pred. No. 8e-11;
Matches 20; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 CKGKGAKSRLMYDCTGSCRSRGK 25

Db 41 CKGKGASCRRTSYDCTGSCRSRGK 65

RESULT 2

Q9NCW6

LD Q9NCV5; PRELIMINARY; PKI; 00 AM.
AC Q9NCV5;
DT 01-OCT-2000 (TRENBLrel. 15, Created)
DT 01-OCT-2000 (TRENBLrel. 15, Last sequence update)
DT 01-JUN-2002 (TRENBLrel. 21, Last annotation update)
DE Four-loop conotoxin (Fragment).

OS Conus catus.
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
OX NCBI_TaxID=101291;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CCATH_R_4;
RA Duda T.F., Palumbi S.R.;
RT "Molecular evolution of four-loop conotoxin precursors from fish-eating Conus."
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF174236; AAF89902.1; -
DR HSSP; P05484; IMVI.
DR InterPro; IPR004214; Conotoxin.
DR Pfam; PF02950; Conotoxin; 1.
FT NON_TER 1
SQ SEQUENCE 66 AA; 7081 MW; 66E4898A6968B31B CRC64;

Query Match 63.2%; Score 120; DB 5; Length 66;
Best Local Similarity 72.0%; Pred. No. 7.9e-10;
Matches 18; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 CKGKGAKCSRLMYDCTGSCRSKGC 25
- - - - -
DB 41 COGRGASCRRTSYDCTGSCRSKGC 65

RESULT 7
Q9NCV7

ID Q9NCV7 PRELIMINARY; PRT; 66 AA.
AC Q9NCV7;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Four-loop conotoxin (Fragment).
OS Conus catus.
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
OX NCBI_TaxID=101291;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CCATH_R_2;
RA Duda T.F., Palumbi S.R.;
RT "Molecular evolution of four-loop conotoxin precursors from fish-eating Conus."
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF174236; AAF89900.1; -
DR HSSP; P05484; IMVI.
DR InterPro; IPR004214; Conotoxin.
DR Pfam; PF02950; Conotoxin; 1.
FT NON_TER 1
SQ SEQUENCE 66 AA; 7053 MW; 7453798A6968B31B CRC64;

Query Match 61.6%; Score 117; DB 5; Length 66;
Best Local Similarity 68.0%; Pred. No. 2.1e-09;
Matches 17; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 1 CKGKGAKCSRLMYDCTGSCRSKGC 25
- - - - -
DB 41 COGRGASCRRTSYDCTGSCRSKGC 65

RESULT 8
Q9N6N6

ID Q9N6N6 PRELIMINARY; PRT; 66 AA.
AC Q9N6N6;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Four-loop conotoxin precursor (Fragment).
OS Conus striatus (Striated cone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.

OX NCBI_TaxID=6493;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CSTRH_L_5, AND CSTRH_L_1;
RA Duda T.F., Palumbi S.R.;
RT "Molecular evolution of four-loop conotoxin precursors from fish-eating Conus."
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF174244; AAF89908.1; -
DR EMBL; AF174240; AAF89904.1; -
DR HSSP; P05484; IMVI.
DR InterPro; IPR004214; Conotoxin.
DR Pfam; PF02950; Conotoxin; 1.
FT NON_TER 1
SQ SEQUENCE 66 AA; 6966 MW; 29A992710CA7DA05 CRC64;

Query Match 61.1%; Score 116; DB 5; Length 66;
Best Local Similarity 72.0%; Pred. No. 2.9e-09;
Matches 18; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 CKGKGAKCSRLMYDCTGSCRSKGC 25
- - - - -
DB 41 CRAAGKSCSRIAYNCTGSCRSKGC 65

RESULT 9
Q9NCV4

ID Q9NCV4 PRELIMINARY; PRT; 66 AA.
AC Q9NCV4;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Four-loop conotoxin (Fragment).
OS Conus striatus (Striated cone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
OX NCBI_TaxID=6493;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CSTRH_L_2;
RA Duda T.F., Palumbi S.R.;
RT "Molecular evolution of four-loop conotoxin precursors from fish-eating Conus."
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF174241; AAF89905.1; -
DR HSSP; P05484; IMVI.
DR InterPro; IPR004214; Conotoxin.
DR Pfam; PF02950; Conotoxin; 1.
FT NON_TER 1
SQ SEQUENCE 66 AA; 6980 MW; 286F491D7CA7DA05 CRC64;

Query Match 61.1%; Score 116; DB 5; Length 66;
Best Local Similarity 72.0%; Pred. No. 2.9e-09;
Matches 18; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 CKGKGAKCSRLMYDCTGSCRSKGC 25
- - - - -
DB 41 CRAAGKSCSRIAYNCTGSCRSKGC 65

RESULT 10
Q9NCV0

ID Q9NCV0 PRELIMINARY; PRT; 66 AA.
AC Q9NCV0;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Four-loop conotoxin (Fragment).
OS Conus striatus (Striated cone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
OX NCBI_TaxID=6493;
RN [1]

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RP SEQUENCE FROM N.A.
RC STRAIN=CSTRH_117;
RA Duda T.F., Palumbi S.R.;
RT "Molecular evolution of four-loop conotoxin precursors from fish-
eating Conus.";
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF174229; AAF89893.1; -.
DR EMBL; AF174226; AAF89890.1; -.
DR HSSP; P05484; 1MWI.
DR InterPro; IPR004214; Conotoxin.
DR Pfam; PF02950; Conotoxin; 1.
FT NON_TER 1
SQ SEQUENCE 66 AA; 6981 MW; 20CDC33D7CA7DA05 CRC64;

Query Match 61.1%; Score 116; DB 5; Length 66;
Best Local Similarity 72.0%; Pred. No. 2.9e-09;
Matches 18; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 CKGKGAKCSRLMYDCTGCSRSGKC 25
II I III :|:|:|:|:|:|:|
DB 41 CKAAGKCSRIAYNCTGCSRSGKC 65

RESULT 11
Q9NCU1 PRELIMINARY; PRT; 66 AA.
AC Q9NCU1;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Four-loop conotoxin (Fragment).
OS Conus striatus (Striated cone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
OX NCBI_TaxID=6493;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CSTRH_11;
RA Duda T.F., Palumbi S.R.;
RT "Molecular evolution of four-loop conotoxin precursors from fish-
eating Conus.";
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF174267; AAF89931.1; -.
DR HSSP; P05484; 1MWI.
DR InterPro; IPR004214; Conotoxin.
DR Pfam; PF02950; Conotoxin; 1.
FT NON_TER 1
SQ SEQUENCE 66 AA; 6951 MW; 0D9868C0A7A1A39F CRC64;

Query Match 61.1%; Score 116; DB 5; Length 66;
Best Local Similarity 72.0%; Pred. No. 2.9e-09;
Matches 18; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 CKGKGAKCSRLMYDCTGCSRSGKC 25
II I III :|:|:|:|:|:|:|
DB 41 CKAAGKCSRIAYNCTGCSRSGKC 65

RESULT 12
Q9NC28 PRELIMINARY; PRT; 66 AA.
AC Q9NC28;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Four-loop conotoxin precursor (Fragment).
OS Conus catus.
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
OX NCBI_TaxID=101291;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CCATH_111_9, AND CCATH_111_6;
RA Duda T.F., Palumbi S.R.;

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RT "Molecular evolution of four-loop conotoxin precursors from fish-
eating Conus.";
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF174229; AAF89893.1; -.
DR EMBL; AF174226; AAF89890.1; -.
DR HSSP; P05484; 1MWI.
DR InterPro; IPR004214; Conotoxin.
DR Pfam; PF02950; Conotoxin; 1.
FT NON_TER 1
SQ SEQUENCE 66 AA; 7057 MW; E7AA5E310968B7DA CRC64;

Query Match 60.5%; Score 115; DB 5; Length 66;
Best Local Similarity 72.0%; Pred. No. 4e-09;
Matches 18; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 1 CKGKGAKCSRLMYDCTGCSRSGKC 25
II I III :|:|:|:|:|:|:|
DB 41 CKSTGASCRRTSYDCTGCSRSGKC 65

RESULT 13
Q9N625 PRELIMINARY; PRT; 66 AA.
AC Q9N625;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Four-loop conotoxin precursor (Fragment).
OS Conus catus.
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
OX NCBI_TaxID=101291;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-VARIOUS STRAINS;
RA Duda T.F., Palumbi S.R.;
RT "Molecular evolution of four-loop conotoxin precursors from fish-
eating Conus.";
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF174228; AAF89892.1; -.
DR EMBL; AF174221; AAF89885.1; -.
DR EMBL; AF174222; AAF89886.1; -.
DR EMBL; AF174224; AAF89888.1; -.
DR EMBL; AF174225; AAF89889.1; -.
DR HSSP; P05484; 1MWI.
DR InterPro; IPR004214; Conotoxin.
DR Pfam; PF02950; Conotoxin; 1.
FT NON_TER 1
SQ SEQUENCE 66 AA; 7056 MW; EAll338A6968B7DA CRC64;

Query Match 60.5%; Score 115; DB 5; Length 66;
Best Local Similarity 72.0%; Pred. No. 4e-09;
Matches 18; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 1 CKGKGAKCSRLMYDCTGCSRSGKC 25
II I III :|:|:|:|:|:|:|
DB 41 CKSTGASCRRTSYDCTGCSRSGKC 65

RESULT 14
Q9NCW2 PRELIMINARY; PRT; 66 AA.
AC Q9NCW2;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Four-loop conotoxin (Fragment).
OS Conus catus.
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
OX NCBI_TaxID=101291;
RN [1]
RP SEQUENCE FROM N.A.

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RC STRAIN-CCATH_111_3;
RA Duda T.F., Palumbi S.R.;
RT "Molecular evolution of four-loop conotoxin precursors from fish-
   eating Conus.";
RL Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AF174223; AAF89887.1; -.
DR HSSP; P05484; LMVI.
DR InterPro; IPR004214; Conotoxin.
DR Pfam; PF02950; Conotoxin; 1.
FT NON_TER 1
SQ SEQUENCE 66 AA; 7026 MW; EA11339E382DB7DA CRC64;

Query Match 60.5%; Score 115; DB 5; Length 66;
Best Local Similarity 72.0%; Pred. No. 4e-09;
Matches 18; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 1 CKGKGAKCSRLMYDCTGSCRSKGC 25
DB 41 CKSTGASCRRTSYDCTGSCRSKGC 65

RESULT 15
Q9NCV3 PRELIMINARY; PRT; 66 AA.
ID Q9NCV3
AC Q9NCV3;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE Four-loop conotoxin (Fragment).
OS Conus striatus (Striated cone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
OX NCBI_TaxID=6493;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-CSTRH_1_3;
RA Duda T.F., Palumbi S.R.;
RT "Molecular evolution of four-loop conotoxin precursors from fish-
   eating Conus.";
RL Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AF174242; AAF89906.1; -.
DR HSSP; P05484; LMVI.
DR InterPro; IPR004214; Conotoxin.
DR Pfam; PF02950; Conotoxin; 1.
FT NON_TER 1
SQ SEQUENCE 66 AA; 7019 MW; 89B89B7AF1A7C7B3 CRC64;

Query Match 60.5%; Score 115; DB 5; Length 66;
Best Local Similarity 72.0%; Pred. No. 4e-09;
Matches 18; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 CKGKGAKCSRLMYDCTGSCRSKGC 25
DB 41 CRAAGKPCSRIAYNCTGSCRSKGC 65
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Search completed: March 17, 2003, 07:26:21
Job time : 29.0916 secs

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